



## SEQUENCE LISTING

RECEIVED  
DEC 03 2002  
TECH CENTER 1600/2900

<110> Zhou, Xiula X. Z.

<120> MODULATORS OF LEUKOCYTE ACTIVATION, COMPOSITIONS AND METHODS OF USE

<130> A-70224/RMS/DHR

<140> US 10/039,761

<141> 2001-10-19

<150> US 60/280,698

<151> 2001-03-29

<160> 5

<170> PatentIn version 3.1

<210> 1

<211> 3955

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1473)..(1473)

<223> "n" at position 1473 can be any base.

<220>

<221> CDS

<222> (355)..(3522)

<223>

<400> 1

cggcagcaaa ggaacgtgcg aacgcgtgac gccgcccgcac tggctcgcgc tctcccgtgc 60

cccggcgctcc tccgcccgt catggcccgg gccgcgcgag acgagcggcg ctgagggcggg 120

ccgcgtggag acgtgaggcg gccgcgtgg cctcacagt cggcgtttcg ccgcctgccc 180

gcggtgcccg cgcacgcctg ccgccatcgc cttcgcgcct ggctggcggg ggcgctgtcc 240

tcccaggccg tccgcgccgc tccctggagc tcggcggagc gcggcagcca gggccggcgg 300

aggcgcgagg agccgggcgc caccgcgcgc gccgcgcgcg ccgcgcggg gggc atg 357

Met

1

acc gtg gag cag aac gtg ctg cag cag agc gcg gcg cag aag cac cag 405

Thr Val Glu Gln Asn Val Leu Gln Gln Ser Ala Ala Gln Lys His Gln

5 10 15

cag acg ttt ttg aat caa ctg aga gaa att acg ggg att aat gac acc 453

Gln Thr Phe Leu Asn Gln Leu Arg Glu Ile Thr Gly Ile Asn Asp Thr

20 25 30

cag ata cta cag caa gcc ttg aag gat agt aat gga aac ttg gaa tta Gln Ile Leu Gln Gln Ala Leu Lys Asp Ser Asn Gly Asn Leu Glu Leu 35 40 45	501
gca gtg gct ttc ctt act gcg aag aat gct aag acc cct cag cag gag Ala Val Ala Phe Leu Thr Ala Lys Asn Ala Lys Thr Pro Gln Gln Glu 50 55 60 65	549
gag aca act tac tac caa aca gca ctt cct ggc aat gat aga tac atc Glu Thr Thr Tyr Tyr Gln Thr Ala Leu Pro Gly Asn Asp Arg Tyr Ile 70 75 80	597
agt gtg gga agc caa gca gat aca aat gtg att gat ctc act gga gat Ser Val Gly Ser Gln Ala Asp Thr Asn Val Ile Asp Leu Thr Gly Asp 85 90 95	645
gat aaa gat gat ctt cag aga aca att gcc ttg agt ttg gcc gaa tca Asp Lys Asp Asp Leu Gln Arg Thr Ile Ala Leu Ser Leu Ala Glu Ser 100 105 110	693
aac agg gca ttc agg gag act gga ata act gat gag gaa caa gcc att Asn Arg Ala Phe Arg Glu Thr Gly Ile Thr Asp Glu Glu Gln Ala Ile 115 120 125	741
agc aga gtt ctt gaa gcc agt ata gca gag aat aaa gca tgt ttg aag Ser Arg Val Leu Glu Ala Ser Ile Ala Glu Asn Lys Ala Cys Leu Lys 130 135 140 145	789
agg aca cct aca gaa gtt tgg agg gat tct cga aac cct tat gat aga Arg Thr Pro Thr Glu Val Trp Arg Asp Ser Arg Asn Pro Tyr Asp Arg 150 155 160	837
aaa aga cag gac aaa gct ccc gtt ggg cta aag aat gtt ggc aat act Lys Arg Gln Asp Lys Ala Pro Val Gly Leu Lys Asn Val Gly Asn Thr 165 170 175	885
tgt tgg ttt agt gct gtt att cag tca tta ttt aat ctt ttg gaa ttt Cys Trp Phe Ser Ala Val Ile Gln Ser Leu Phe Asn Leu Leu Glu Phe 180 185 190	933
aga aga tta gtt ctg aat tac aag cct cca tca aat gct caa gat tta Arg Arg Leu Val Leu Asn Tyr Lys Pro Pro Ser Asn Ala Gln Asp Leu 195 200 205	981
ccc cga aac caa aag gaa cat cgg aat ttg cct ttt atg cgt gag ctg Pro Arg Asn Gln Lys Glu His Arg Asn Leu Pro Phe Met Arg Glu Leu 210 215 220 225	1029
agg tat cta ttt gca ctt ctt gtt ggt acc aaa agg aag tat gtt gat Arg Tyr Leu Phe Ala Leu Leu Val Gly Thr Lys Arg Lys Tyr Val Asp 230 235 240	1077
cca tca aga gca gtt gaa att ctt aag gat gct ttc aaa tca aat gac Pro Ser Arg Ala Val Glu Ile Leu Lys Asp Ala Phe Lys Ser Asn Asp 245 250 255	1125

tca cag cag caa gat gtg agt gag ttt aca cac aaa tta tta gat tgg	1173
Ser Gln Gln Gln Asp Val Ser Glu Phe Thr His Lys Leu Leu Asp Trp	
260 265 270	
tta gaa gat gcc ttc caa atg aaa gct gaa gag gag acg gat gaa gag	1221
Leu Glu Asp Ala Phe Gln Met Lys Ala Glu Glu Glu Thr Asp Glu Glu	
275 280 285	
aag cca aag aac ccc atg gta gag ttg ttc tat ggc aga ttc ctg gct	1269
Lys Pro Lys Asn Pro Met Val Glu Leu Phe Tyr Gly Arg Phe Leu Ala	
290 295 300 305	
gtg gga gta ctt gaa ggt aaa aaa ttt gaa aac act gaa atg ttt ggt	1317
Val Gly Val Leu Glu Gly Lys Lys Phe Glu Asn Thr Glu Met Phe Gly	
310 315 320	
cag tac cca ctt cag gtc aat ggg ttc aaa gat ctg cat gag tgc cta	1365
Gln Tyr Pro Leu Gln Val Asn Gly Phe Lys Asp Leu His Glu Cys Leu	
325 330 335	
gaa gct gca atg att gaa gga gaa att gag tct tta cat tca gag aat	1413
Glu Ala Ala Met Ile Glu Gly Glu Ile Glu Ser Leu His Ser Glu Asn	
340 345 350	
tca gga aaa tca ggc caa gag cat tgg ttt act gga tta cca cct gtg	1461
Ser Gly Lys Ser Gly Gln Glu His Trp Phe Thr Gly Leu Pro Pro Val	
355 360 365	
tta aca ttt gan ttg tca aga ttt gaa ttt aat cag gca ttg gga aga	1509
Leu Thr Phe Xaa Leu Ser Arg Phe Glu Phe Asn Gln Ala Leu Gly Arg	
370 375 380 385	
cca gaa aaa att cac aac aaa tta gaa ttt ccc caa gtt tta tat ttg	1557
Pro Glu Lys Ile His Asn Lys Leu Glu Phe Pro Gln Val Leu Tyr Leu	
390 395 400	
gac aga tac atg cac aga aac aga gaa ata aca aga att aag agg gaa	1605
Asp Arg Tyr Met His Arg Asn Arg Glu Ile Thr Arg Ile Lys Arg Glu	
405 410 415	
gag atc aag aga ctg aaa gat tac ctc acg gta tta caa caa agg cta	1653
Glu Ile Lys Arg Leu Lys Asp Tyr Leu Thr Val Leu Gln Gln Arg Leu	
420 425 430	
gaa aga tat tta agc tat ggt tcc ggt ccc aaa cga ttc ccc ttg gta	1701
Glu Arg Tyr Leu Ser Tyr Gly Ser Gly Pro Lys Arg Phe Pro Leu Val	
435 440 445	
gat gtt ctt cag tat gca ttg gaa ttt gcc tca agt aaa cct gtt tgc	1749
Asp Val Leu Gln Tyr Ala Leu Glu Phe Ala Ser Ser Lys Pro Val Cys	
450 455 460 465	
act tct cct gtt gac gat att gac gct agt tcc cca cct agt ggt tcc	1797
Thr Ser Pro Val Asp Asp Ile Asp Ala Ser Ser Pro Pro Ser Gly Ser	
470 475 480	
ata cca tca cag aca tta cca agc aca aca gaa caa cag gga gcc cta	1845

Ile	Pro	Ser	Gln	Thr	Leu	Pro	Ser	Thr	Thr	Glu	Gln	Gln	Gly	Ala	Leu		
			485					490					495				
tct	tca	gaa	ctg	cca	agc	aca	tca	cct	tca	tca	gtt	gct	gcc	att	tca	1893	
Ser	Ser	Glu	Leu	Pro	Ser	Thr	Ser	Pro	Ser	Ser	Val	Ala	Ala	Ile	Ser		
		500					505					510					
tcg	aga	tca	gta	ata	cac	aaa	cca	ttt	act	cag	tcc	cgg	ata	cct	cca	1941	
Ser	Arg	Ser	Val	Ile	His	Lys	Pro	Phe	Thr	Gln	Ser	Arg	Ile	Pro	Pro		
	515					520					525						
gat	ttg	ccc	atg	cat	ccg	gca	cca	agg	cac	ata	acg	gag	gaa	gaa	ctt	1989	
Asp	Leu	Pro	Met	His	Pro	Ala	Pro	Arg	His	Ile	Thr	Glu	Glu	Glu	Leu		
530					535					540					545		
tct	gtg	ctg	gaa	agt	tgt	tta	cat	cgc	tgg	agg	aca	gaa	ata	gaa	aat	2037	
Ser	Val	Leu	Glu	Ser	Cys	Leu	His	Arg	Trp	Arg	Thr	Glu	Ile	Glu	Asn		
				550					555						560		
gac	acc	aga	gat	ttg	cag	gaa	agc	ata	tcc	aga	atc	cat	cga	aca	att	2085	
Asp	Thr	Arg	Asp	Leu	Gln	Glu	Ser	Ile	Ser	Arg	Ile	His	Arg	Thr	Ile		
			565					570					575				
gaa	tta	atg	tac	tct	gac	aaa	tct	atg	ata	caa	gtt	cct	tat	cga	tta	2133	
Glu	Leu	Met	Tyr	Ser	Asp	Lys	Ser	Met	Ile	Gln	Val	Pro	Tyr	Arg	Leu		
		580					585					590					
cat	gcc	gtt	tta	gtt	cac	gaa	ggc	caa	gct	aat	gct	ggg	cac	tac	tgg	2181	
His	Ala	Val	Leu	Val	His	Glu	Gly	Gln	Ala	Asn	Ala	Gly	His	Tyr	Trp		
	595					600					605						
gca	tat	att	ttt	gat	cat	cgt	gaa	agc	aga	tgg	atg	aag	tac	aat	gat	2229	
Ala	Tyr	Ile	Phe	Asp	His	Arg	Glu	Ser	Arg	Trp	Met	Lys	Tyr	Asn	Asp		
610					615					620					625		
att	gct	gtg	aca	aaa	tca	tca	tgg	gaa	gag	cta	gtg	agg	gac	tct	ttt	2277	
Ile	Ala	Val	Thr	Lys	Ser	Ser	Trp	Glu	Glu	Leu	Val	Arg	Asp	Ser	Phe		
				630					635						640		
ggt	ggt	tat	aga	aat	gcc	agt	gca	tac	tgt	tta	atg	tac	ata	aat	gat	2325	
Gly	Gly	Tyr	Arg	Asn	Ala	Ser	Ala	Tyr	Cys	Leu	Met	Tyr	Ile	Asn	Asp		
			645					650					655				
aag	gca	cag	ttc	cta	ata	caa	gag	gag	ttt	aat	aaa	gaa	act	ggg	cag	2373	
Lys	Ala	Gln	Phe	Leu	Ile	Gln	Glu	Glu	Phe	Asn	Lys	Glu	Thr	Gly	Gln		
		660					665					670					
ccc	ctt	gtt	ggt	ata	gaa	aca	tta	cca	ccg	gat	ttg	aga	gat	ttt	gtt	2421	
Pro	Leu	Val	Gly	Ile	Glu	Thr	Leu	Pro	Pro	Asp	Leu	Arg	Asp	Phe	Val		
		675				680					685						
gag	gaa	gac	aac	caa	cga	ttt	gaa	aaa	gaa	cta	gaa	gaa	tgg	gat	gca	2469	
Glu	Glu	Asp	Asn	Gln	Arg	Phe	Glu	Lys	Glu	Leu	Glu	Glu	Trp	Asp	Ala		
690				695					700						705		
caa	ctt	gcc	cag	aaa	gct	ttg	cag	gaa	aag	ctt	tta	gcg	tct	cag	aaa	2517	
Gln	Leu	Ala	Gln	Lys	Ala	Leu	Gln	Glu	Lys	Leu	Leu	Ala	Ser	Gln	Lys		

710	715	720	
ttg aga gag tca gag act tct gtg aca aca gca caa gca gca gga gac Leu Arg Glu Ser Glu Thr Ser Val Thr Thr Ala Gln Ala Ala Gly Asp 725 730 735			2565
cca gaa tat cta gag cag cca tca aga agt gat ttc tca aag cac ttg Pro Glu Tyr Leu Glu Gln Pro Ser Arg Ser Asp Phe Ser Lys His Leu 740 745 750			2613
aaa gaa gaa act att caa ata att acc aag gca tca cat gag cat gaa Lys Glu Glu Thr Ile Gln Ile Ile Thr Lys Ala Ser His Glu His Glu 755 760 765			2661
gat aaa agt cct gaa aca gtt ttg cag tcg gca att aag ttg gaa tat Asp Lys Ser Pro Glu Thr Val Leu Gln Ser Ala Ile Lys Leu Glu Tyr 770 775 780 785			2709
gca agg ttg gtt aag ttg gcc caa gaa gac acc cca cca gaa acc gat Ala Arg Leu Val Lys Leu Ala Gln Glu Asp Thr Pro Pro Glu Thr Asp 790 795 800			2757
tat cgt tta cat cat gta gtg gtc tac ttt atc cag aac cag gca cca Tyr Arg Leu His His Val Val Val Tyr Phe Ile Gln Asn Gln Ala Pro 805 810 815			2805
aag aaa att att gag aaa aca tta cta gaa caa ttt gga gat aga aat Lys Lys Ile Ile Glu Lys Thr Leu Leu Glu Gln Phe Gly Asp Arg Asn 820 825 830			2853
ttg agt ttt gat gaa agg tgt cac aac ata atg aaa gtt gct caa gcc Leu Ser Phe Asp Glu Arg Cys His Asn Ile Met Lys Val Ala Gln Ala 835 840 845			2901
aaa ctg gaa atg ata aaa cct gaa gaa gta aac ttg gag gaa tat gag Lys Leu Glu Met Ile Lys Pro Glu Glu Val Asn Leu Glu Glu Tyr Glu 850 855 860 865			2949
gag tgg cat cag gat tat agg aaa ttc agg gaa aca act atg tat ctc Glu Trp His Gln Asp Tyr Arg Lys Phe Arg Glu Thr Thr Met Tyr Leu 870 875 880			2997
ata att ggg cta gaa aat ttt caa aga gaa agt tat ata gat tcc ttg Ile Ile Gly Leu Glu Asn Phe Gln Arg Glu Ser Tyr Ile Asp Ser Leu 885 890 895			3045
ctg ttc ctc atc tgt gct tat cag aat aac aaa gaa ctc ttg tct aaa Leu Phe Leu Ile Cys Ala Tyr Gln Asn Asn Lys Glu Leu Leu Ser Lys 900 905 910			3093
ggc tta tac aga gga cat gat gaa gaa ttg ata tca cat tat aga aga Gly Leu Tyr Arg Gly His Asp Glu Glu Leu Ile Ser His Tyr Arg Arg 915 920 925			3141
gaa tgt ttg cta aaa tta aat gag caa gcc gca gaa ctc ttc gaa tct Glu Cys Leu Leu Lys Leu Asn Glu Gln Ala Ala Glu Leu Phe Glu Ser 930 935 940 945			3189

gga gag gat cga gaa gta aac aat ggt ttg att atc atg aat gag ttt Gly Glu Asp Arg Glu Val Asn Asn Gly Leu Ile Ile Met Asn Glu Phe 950 955 960	3237
att gtc cca ttt ttg cca tta tta ctg gtg gat gaa atg gaa gaa aag Ile Val Pro Phe Leu Pro Leu Leu Leu Val Asp Glu Met Glu Glu Lys 965 970 975	3285
gat ata cta gct gta gaa gat atg aga aat cga tgg tgt tcc tac ctt Asp Ile Leu Ala Val Glu Asp Met Arg Asn Arg Trp Cys Ser Tyr Leu 980 985 990	3333
ggt caa gaa atg gaa cca cac ctc caa gaa aag ctg aca gat ttt ttg Gly Gln Glu Met Glu Pro His Leu Gln Glu Lys Leu Thr Asp Phe Leu 995 1000 1005	3381
cca aaa ctg ctt gat tgt tct atg gag att aaa agt ttc cat gag Pro Lys Leu Leu Asp Cys Ser Met Glu Ile Lys Ser Phe His Glu 1010 1015 1020	3426
cca ccg aag tta cct tca tat tcc acg cat gaa ctc tgt gag cga Pro Pro Lys Leu Pro Ser Tyr Ser Thr His Glu Leu Cys Glu Arg 1025 1030 1035	3471
ttt gcc cga atc atg ttg tcc ctc agt cga act cct gct gat gga Phe Ala Arg Ile Met Leu Ser Leu Ser Arg Thr Pro Ala Asp Gly 1040 1045 1050	3516
aga taa actgcacact ttcctgaac aactgtata aactcttttt agttcttaac Arg 1055	3572
ccttgcccttc ctgtcacagg gtttgcttgt tgctgctata gtttttaact tttttttatt	3632
ttaataactg caaaagacaa aatgactata cagacttttag tcagactgca gacaataaag	3692
ctgaaaatcg catggcgctc agacatttta accggaactg atgtataatc acaaacttaa	3752
ttgatttttat tatggcaaaa ctatgctttt gccaccttcc tgttgacagta ttactttgct	3812
tttatctttt ctttctcaac agctttccat tcagtctgga tccttccatg actacagcca	3872
tttaagtgtt cagcactgtg tacgatacat aatatttggt agcttgtaaa tgaaataaag	3932
aataaagttt tatttatggc tac	3955

<210> 2

<211> 1055

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (373)..(373)

<223> The 'Xaa' at location 373 stands for Glu, or Asp.

<220>  
 <221> misc\_feature  
 <222> (1473)..(1473)  
 <223> "n" at position 1473 can be any base.

<400> 2

Met Thr Val Glu Gln Asn Val Leu Gln Gln Ser Ala Ala Gln Lys His  
 1 5 10 15

Gln Gln Thr Phe Leu Asn Gln Leu Arg Glu Ile Thr Gly Ile Asn Asp  
 20 25 30

Thr Gln Ile Leu Gln Gln Ala Leu Lys Asp Ser Asn Gly Asn Leu Glu  
 35 40 45

Leu Ala Val Ala Phe Leu Thr Ala Lys Asn Ala Lys Thr Pro Gln Gln  
 50 55 60

Glu Glu Thr Thr Tyr Tyr Gln Thr Ala Leu Pro Gly Asn Asp Arg Tyr  
 65 70 75 80

Ile Ser Val Gly Ser Gln Ala Asp Thr Asn Val Ile Asp Leu Thr Gly  
 85 90 95

Asp Asp Lys Asp Asp Leu Gln Arg Thr Ile Ala Leu Ser Leu Ala Glu  
 100 105 110

Ser Asn Arg Ala Phe Arg Glu Thr Gly Ile Thr Asp Glu Glu Gln Ala  
 115 120 125

Ile Ser Arg Val Leu Glu Ala Ser Ile Ala Glu Asn Lys Ala Cys Leu  
 130 135 140

Lys Arg Thr Pro Thr Glu Val Trp Arg Asp Ser Arg Asn Pro Tyr Asp  
 145 150 155 160

Arg Lys Arg Gln Asp Lys Ala Pro Val Gly Leu Lys Asn Val Gly Asn  
 165 170 175

Thr Cys Trp Phe Ser Ala Val Ile Gln Ser Leu Phe Asn Leu Leu Glu  
 180 185 190

Phe Arg Arg Leu Val Leu Asn Tyr Lys Pro Pro Ser Asn Ala Gln Asp

195	200	205
Leu Pro Arg Asn Gln Lys Glu His Arg Asn Leu Pro Phe Met Arg Glu		
210	215	220
Leu Arg Tyr Leu Phe Ala Leu Leu Val Gly Thr Lys Arg Lys Tyr Val		
225	230	235 240
Asp Pro Ser Arg Ala Val Glu Ile Leu Lys Asp Ala Phe Lys Ser Asn		
	245	250 255
Asp Ser Gln Gln Gln Asp Val Ser Glu Phe Thr His Lys Leu Leu Asp		
	260	265 270
Trp Leu Glu Asp Ala Phe Gln Met Lys Ala Glu Glu Glu Thr Asp Glu		
	275	280 285
Glu Lys Pro Lys Asn Pro Met Val Glu Leu Phe Tyr Gly Arg Phe Leu		
	290	295 300
Ala Val Gly Val Leu Glu Gly Lys Lys Phe Glu Asn Thr Glu Met Phe		
305	310	315 320
Gly Gln Tyr Pro Leu Gln Val Asn Gly Phe Lys Asp Leu His Glu Cys		
	325	330 335
Leu Glu Ala Ala Met Ile Glu Gly Glu Ile Glu Ser Leu His Ser Glu		
	340	345 350
Asn Ser Gly Lys Ser Gly Gln Glu His Trp Phe Thr Gly Leu Pro Pro		
	355	360 365
Val Leu Thr Phe Xaa Leu Ser Arg Phe Glu Phe Asn Gln Ala Leu Gly		
	370	375 380
Arg Pro Glu Lys Ile His Asn Lys Leu Glu Phe Pro Gln Val Leu Tyr		
385	390	395 400
Leu Asp Arg Tyr Met His Arg Asn Arg Glu Ile Thr Arg Ile Lys Arg		
	405	410 415
Glu Glu Ile Lys Arg Leu Lys Asp Tyr Leu Thr Val Leu Gln Gln Arg		
	420	425 430



Leu Glu Arg Tyr Leu Ser Tyr Gly Ser Gly Pro Lys Arg Phe Pro Leu  
435 440 445

Val Asp Val Leu Gln Tyr Ala Leu Glu Phe Ala Ser Ser Lys Pro Val  
450 455 460

Cys Thr Ser Pro Val Asp Asp Ile Asp Ala Ser Ser Pro Pro Ser Gly  
465 470 475 480

Ser Ile Pro Ser Gln Thr Leu Pro Ser Thr Thr Glu Gln Gln Gly Ala  
485 490 495

Leu Ser Ser Glu Leu Pro Ser Thr Ser Pro Ser Ser Val Ala Ala Ile  
500 505 510

Ser Ser Arg Ser Val Ile His Lys Pro Phe Thr Gln Ser Arg Ile Pro  
515 520 525

Pro Asp Leu Pro Met His Pro Ala Pro Arg His Ile Thr Glu Glu Glu  
530 535 540

Leu Ser Val Leu Glu Ser Cys Leu His Arg Trp Arg Thr Glu Ile Glu  
545 550 555 560

Asn Asp Thr Arg Asp Leu Gln Glu Ser Ile Ser Arg Ile His Arg Thr  
565 570 575

Ile Glu Leu Met Tyr Ser Asp Lys Ser Met Ile Gln Val Pro Tyr Arg  
580 585 590

Leu His Ala Val Leu Val His Glu Gly Gln Ala Asn Ala Gly His Tyr  
595 600 605

Trp Ala Tyr Ile Phe Asp His Arg Glu Ser Arg Trp Met Lys Tyr Asn  
610 615 620

Asp Ile Ala Val Thr Lys Ser Ser Trp Glu Glu Leu Val Arg Asp Ser  
625 630 635 640

Phe Gly Gly Tyr Arg Asn Ala Ser Ala Tyr Cys Leu Met Tyr Ile Asn  
645 650 655

Asp Lys Ala Gln Phe Leu Ile Gln Glu Glu Phe Asn Lys Glu Thr Gly  
660 665 670

Gln Pro Leu Val Gly Ile Glu Thr Leu Pro Pro Asp Leu Arg Asp Phe  
675 680 685

Val Glu Glu Asp Asn Gln Arg Phe Glu Lys Glu Leu Glu Glu Trp Asp  
690 695 700

Ala Gln Leu Ala Gln Lys Ala Leu Gln Glu Lys Leu Leu Ala Ser Gln  
705 710 715 720

Lys Leu Arg Glu Ser Glu Thr Ser Val Thr Thr Ala Gln Ala Ala Gly  
725 730 735

Asp Pro Glu Tyr Leu Glu Gln Pro Ser Arg Ser Asp Phe Ser Lys His  
740 745 750

Leu Lys Glu Glu Thr Ile Gln Ile Ile Thr Lys Ala Ser His Glu His  
755 760 765

Glu Asp Lys Ser Pro Glu Thr Val Leu Gln Ser Ala Ile Lys Leu Glu  
770 775 780

Tyr Ala Arg Leu Val Lys Leu Ala Gln Glu Asp Thr Pro Pro Glu Thr  
785 790 795 800

Asp Tyr Arg Leu His His Val Val Val Tyr Phe Ile Gln Asn Gln Ala  
805 810 815

Pro Lys Lys Ile Ile Glu Lys Thr Leu Leu Glu Gln Phe Gly Asp Arg  
820 825 830

Asn Leu Ser Phe Asp Glu Arg Cys His Asn Ile Met Lys Val Ala Gln  
835 840 845

Ala Lys Leu Glu Met Ile Lys Pro Glu Glu Val Asn Leu Glu Glu Tyr  
850 855 860

Glu Glu Trp His Gln Asp Tyr Arg Lys Phe Arg Glu Thr Thr Met Tyr  
865 870 875 880

Leu Ile Ile Gly Leu Glu Asn Phe Gln Arg Glu Ser Tyr Ile Asp Ser  
885 890 895

Leu Leu Phe Leu Ile Cys Ala Tyr Gln Asn Asn Lys Glu Leu Leu Ser  
900 905 910

Lys Gly Leu Tyr Arg Gly His Asp Glu Glu Leu Ile Ser His Tyr Arg  
915 920 925

Arg Glu Cys Leu Leu Lys Leu Asn Glu Gln Ala Ala Glu Leu Phe Glu  
930 935 940

Ser Gly Glu Asp Arg Glu Val Asn Asn Gly Leu Ile Ile Met Asn Glu  
945 950 955 960

Phe Ile Val Pro Phe Leu Pro Leu Leu Leu Val Asp Glu Met Glu Glu  
965 970 975

Lys Asp Ile Leu Ala Val Glu Asp Met Arg Asn Arg Trp Cys Ser Tyr  
980 985 990

Leu Gly Gln Glu Met Glu Pro His Leu Gln Glu Lys Leu Thr Asp Phe  
995 1000 1005

Leu Pro Lys Leu Leu Asp Cys Ser Met Glu Ile Lys Ser Phe His  
1010 1015 1020

Glu Pro Pro Lys Leu Pro Ser Tyr Ser Thr His Glu Leu Cys Glu  
1025 1030 1035

Arg Phe Ala Arg Ile Met Leu Ser Leu Ser Arg Thr Pro Ala Asp  
1040 1045 1050

Gly Arg  
1055

<210> 3  
<211> 4015  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1473)..(1473)  
<223> "n" at position 1473 can be any base.

<220>  
 <221> CDS  
 <222> (355) .. (3582)  
 <223>

<400> 3  
 cggcagcaaa ggaacgtgcg aacgcgtgac gccgcccgcac tggctcgcg tctcccgtgc 60  
 cccggcgctcc tccgcccgt catggcccgg gccgcccgcg acgagcggcg ctgaggcggg 120  
 ccgcgtggag acgtgaggcg gccgcctgg ccctcacagt cggcgtttcg ccgcctgccc 180  
 gcggtgcccc cgcacgcctg ccgccatcgc cttcgcgctt ggctggcggg ggcgctgtcc 240  
 tcccaggccg tccgcgccgc tccctggagc tcggcggagc gcggcagcca gggccggcgg 300  
 aggcgcgagg agccggggcg caccgcgcgc gccgcccgc cgcgcgcggg ggcc atg 357  
 Met  
 1  
 acc gtg gag cag aac gtg ctg cag cag agc gcg gcg cag aag cac cag 405  
 Thr Val Glu Gln Asn Val Leu Gln Gln Ser Ala Ala Gln Lys His Gln  
 5 10 15  
 cag acg ttt ttg aat caa ctg aga gaa att acg ggg att aat gac acc 453  
 Gln Thr Phe Leu Asn Gln Leu Arg Glu Ile Thr Gly Ile Asn Asp Thr  
 20 25 30  
 cag ata cta cag caa gcc ttg aag gat agt aat gga aac ttg gaa tta 501  
 Gln Ile Leu Gln Gln Ala Leu Lys Asp Ser Asn Gly Asn Leu Glu Leu  
 35 40 45  
 gca gtg gct ttc ctt act gcg aag aat gct aag acc cct cag cag gag 549  
 Ala Val Ala Phe Leu Thr Ala Lys Asn Ala Lys Thr Pro Gln Gln Glu  
 50 55 60 65  
 gag aca act tac tac caa aca gca ctt cct ggc aat gat aga tac atc 597  
 Glu Thr Thr Tyr Tyr Gln Thr Ala Leu Pro Gly Asn Asp Arg Tyr Ile  
 70 75 80  
 agt gtg gga agc caa gca gat aca aat gtg att gat ctc act gga gat 645  
 Ser Val Gly Ser Gln Ala Asp Thr Asn Val Ile Asp Leu Thr Gly Asp  
 85 90 95  
 gat aaa gat gat ctt cag aga aca att gcc ttg agt ttg gcc gaa tca 693  
 Asp Lys Asp Asp Leu Gln Arg Thr Ile Ala Leu Ser Leu Ala Glu Ser  
 100 105 110  
 aac agg gca ttc agg gag act gga ata act gat gag gaa caa gcc att 741  
 Asn Arg Ala Phe Arg Glu Thr Gly Ile Thr Asp Glu Glu Gln Ala Ile  
 115 120 125  
 agc aga gtt ctt gaa gcc agt ata gca gag aat aaa gca tgt ttg aag 789  
 Ser Arg Val Leu Glu Ala Ser Ile Ala Glu Asn Lys Ala Cys Leu Lys

130	135	140	145	
agg aca cct aca gaa gtt tgg agg gat tct cga aac cct tat gat aga				837
Arg Thr Pro Thr Glu Val Trp Arg Asp Ser Arg Asn Pro Tyr Asp Arg				
	150	155	160	
aaa aga cag gac aaa gct ccc gtt ggg cta aag aat gtt ggc aat act				885
Lys Arg Gln Asp Lys Ala Pro Val Gly Leu Lys Asn Val Gly Asn Thr				
	165	170	175	
tgt tgg ttt agt gct gtt att cag tca tta ttt aat ctt ttg gaa ttt				933
Cys Trp Phe Ser Ala Val Ile Gln Ser Leu Phe Asn Leu Leu Glu Phe				
	180	185	190	
aga aga tta gtt ctg aat tac aag cct cca tca aat gct caa gat tta				981
Arg Arg Leu Val Leu Asn Tyr Lys Pro Pro Ser Asn Ala Gln Asp Leu				
	195	200	205	
ccc cga aac caa aag gaa cat cgg aat ttg cct ttt atg cgt gag ctg				1029
Pro Arg Asn Gln Lys Glu His Arg Asn Leu Pro Phe Met Arg Glu Leu				
	210	215	220	225
agg tat cta ttt gca ctt ctt gtt ggt acc aaa agg aag tat gtt gat				1077
Arg Tyr Leu Phe Ala Leu Leu Val Gly Thr Lys Arg Lys Tyr Val Asp				
	230	235	240	
cca tca aga gca gtt gaa att ctt aag gat gct ttc aaa tca aat gac				1125
Pro Ser Arg Ala Val Glu Ile Leu Lys Asp Ala Phe Lys Ser Asn Asp				
	245	250	255	
tca cag cag caa gat gtg agt gag ttt aca cac aaa tta tta gat tgg				1173
Ser Gln Gln Gln Asp Val Ser Glu Phe Thr His Lys Leu Leu Asp Trp				
	260	265	270	
tta gaa gat gcc ttc caa atg aaa gct gaa gag gag acg gat gaa gag				1221
Leu Glu Asp Ala Phe Gln Met Lys Ala Glu Glu Glu Thr Asp Glu Glu				
	275	280	285	
aag cca aag aac ccc atg gta gag ttg ttc tat ggc aga ttc ctg gct				1269
Lys Pro Lys Asn Pro Met Val Glu Leu Phe Tyr Gly Arg Phe Leu Ala				
	290	295	300	305
gtg gga gta ctt gaa ggt aaa aaa ttt gaa aac act gaa atg ttt ggt				1317
Val Gly Val Leu Glu Gly Lys Lys Phe Glu Asn Thr Glu Met Phe Gly				
	310	315	320	
cag tac cca ctt cag gtc aat ggg ttc aaa gat ctg cat gag tgc cta				1365
Gln Tyr Pro Leu Gln Val Asn Gly Phe Lys Asp Leu His Glu Cys Leu				
	325	330	335	
gaa gct gca atg att gaa gga gaa att gag tct tta cat tca gag aat				1413
Glu Ala Ala Met Ile Glu Gly Glu Ile Glu Ser Leu His Ser Glu Asn				
	340	345	350	
tca gga aaa tca ggc caa gag cat tgg ttt act gga tta cca cct gtg				1461
Ser Gly Lys Ser Gly Gln Glu His Trp Phe Thr Gly Leu Pro Pro Val				
	355	360	365	

tta aca ttt gan ttg tca aga ttt gaa ttt aat cag gca ttg gga aga	1509
Leu Thr Phe Xaa Leu Ser Arg Phe Glu Phe Asn Gln Ala Leu Gly Arg	
370 375 380 385	
cca gaa aaa att cac aac aaa tta gaa ttt ccc caa gtt tta tat ttg	1557
Pro Glu Lys Ile His Asn Lys Leu Glu Phe Pro Gln Val Leu Tyr Leu	
390 395 400	
gac aga tac atg cac aga aac aga gaa ata aca aga att aag agg gaa	1605
Asp Arg Tyr Met His Arg Asn Arg Glu Ile Thr Arg Ile Lys Arg Glu	
405 410 415	
gag atc aag aga ctg aaa gat tac ctc acg gta tta caa caa agg cta	1653
Glu Ile Lys Arg Leu Lys Asp Tyr Leu Thr Val Leu Gln Gln Arg Leu	
420 425 430	
gaa aga tat tta agc tat ggt tcc ggt ccc aaa cga ttc ccc ttg gta	1701
Glu Arg Tyr Leu Ser Tyr Gly Ser Gly Pro Lys Arg Phe Pro Leu Val	
435 440 445	
gat gtt ctt cag tat gca ttg gaa ttt gcc tca agt aaa cct gtt tgc	1749
Asp Val Leu Gln Tyr Ala Leu Glu Phe Ala Ser Ser Lys Pro Val Cys	
450 455 460 465	
act tct cct gtt gac gat att gac gct agt tcc cca cct agt ggt tcc	1797
Thr Ser Pro Val Asp Asp Ile Asp Ala Ser Ser Pro Pro Ser Gly Ser	
470 475 480	
ata cca tca cag aca tta cca agc aca aca gaa caa cag gga gcc cta	1845
Ile Pro Ser Gln Thr Leu Pro Ser Thr Thr Glu Gln Gln Gly Ala Leu	
485 490 495	
tct tca gaa ctg cca agc aca tca cct tca tca gtt gct gcc att tca	1893
Ser Ser Glu Leu Pro Ser Thr Ser Pro Ser Ser Val Ala Ala Ile Ser	
500 505 510	
tcg aga tca gta ata cac aaa cca ttt act cag tcc cgg ata cct cca	1941
Ser Arg Ser Val Ile His Lys Pro Phe Thr Gln Ser Arg Ile Pro Pro	
515 520 525	
gat ttg ccc atg cat ccg gca cca agg cac ata acg gag gaa gaa ctt	1989
Asp Leu Pro Met His Pro Ala Pro Arg His Ile Thr Glu Glu Glu Leu	
530 535 540 545	
tct gtg ctg gaa agt tgt tta cat cgc tgg agg aca gaa ata gaa aat	2037
Ser Val Leu Glu Ser Cys Leu His Arg Trp Arg Thr Glu Ile Glu Asn	
550 555 560	
gac acc aga gat ttg cag gaa agc ata tcc aga atc cat cga aca att	2085
Asp Thr Arg Asp Leu Gln Glu Ser Ile Ser Arg Ile His Arg Thr Ile	
565 570 575	
gaa tta atg tac tct gac aaa tct atg ata caa gtt cct tat cga tta	2133
Glu Leu Met Tyr Ser Asp Lys Ser Met Ile Gln Val Pro Tyr Arg Leu	
580 585 590	

cat gcc gtt tta gtt cac gaa ggc caa gct aat gct ggg cac tac tgg	2181
His Ala Val Leu Val His Glu Gly Gln Ala Asn Ala Gly His Tyr Trp	
595 600 605	
gca tat att ttt gat cat cgt gaa agc aga tgg atg aag tac aat gat	2229
Ala Tyr Ile Phe Asp His Arg Glu Ser Arg Trp Met Lys Tyr Asn Asp	
610 615 620 625	
att gct gtg aca aaa tca tca tgg gaa gag cta gtg agg gac tct ttt	2277
Ile Ala Val Thr Lys Ser Ser Trp Glu Glu Leu Val Arg Asp Ser Phe	
630 635 640	
ggg ggt tat aga aat gcc agt gca tac tgt tta atg tac ata aat gat	2325
Gly Gly Tyr Arg Asn Ala Ser Ala Tyr Cys Leu Met Tyr Ile Asn Asp	
645 650 655	
aag gca cag ttc cta ata caa gag gag ttt aat aaa gaa act ggg cag	2373
Lys Ala Gln Phe Leu Ile Gln Glu Glu Phe Asn Lys Glu Thr Gly Gln	
660 665 670	
ccc ctt gtt ggt ata gaa aca tta cca ccg gat ttg aga gat ttt gtt	2421
Pro Leu Val Gly Ile Glu Thr Leu Pro Pro Asp Leu Arg Asp Phe Val	
675 680 685	
gag gaa gac aac caa cga ttt gaa aaa gaa cta gaa gaa tgg gat gca	2469
Glu Glu Asp Asn Gln Arg Phe Glu Lys Glu Leu Glu Glu Trp Asp Ala	
690 695 700 705	
caa ctt gcc cag aaa gct ttg cag gaa aag ctt tta gcg tct cag aaa	2517
Gln Leu Ala Gln Lys Ala Leu Gln Glu Lys Leu Leu Ala Ser Gln Lys	
710 715 720	
ttg aga gag tca gag act tct gtg aca aca gca caa gca gca gga gac	2565
Leu Arg Glu Ser Glu Thr Ser Val Thr Thr Ala Gln Ala Ala Gly Asp	
725 730 735	
cca gaa tat cta gag cag cca tca aga agt gat ttc tca aag cac ttg	2613
Pro Glu Tyr Leu Glu Gln Pro Ser Arg Ser Asp Phe Ser Lys His Leu	
740 745 750	
aaa gaa gaa act att caa ata att acc aag gca tca cat gag cat gaa	2661
Lys Glu Glu Thr Ile Gln Ile Ile Thr Lys Ala Ser His Glu His Glu	
755 760 765	
gat aaa agt cct gaa aca gtt ttg cag tcg gca att aag ttg gaa tat	2709
Asp Lys Ser Pro Glu Thr Val Leu Gln Ser Ala Ile Lys Leu Glu Tyr	
770 775 780 785	
gca agg ttg gtt aag ttg gcc caa gaa gac acc cca cca gaa acc gat	2757
Ala Arg Leu Val Lys Leu Ala Gln Glu Asp Thr Pro Pro Glu Thr Asp	
790 795 800	
tat cgt tta cat cat gta gtg gtc tac ttt atc cag aac cag gca cca	2805
Tyr Arg Leu His His Val Val Val Tyr Phe Ile Gln Asn Gln Ala Pro	
805 810 815	
aag aaa att att gag aaa aca tta cta gaa caa ttt gga gat aga aat	2853

Lys Lys Ile Ile Glu Lys Thr Leu Leu Glu Gln Phe Gly Asp Arg Asn	
820 825 830	
ttg agt ttt gat gaa agg tgt cac aac ata atg aaa gtt gct caa gcc	2901
Leu Ser Phe Asp Glu Arg Cys His Asn Ile Met Lys Val Ala Gln Ala	
835 840 845	
aaa ctg gaa atg ata aaa cct gaa gaa gta aac ttg gag gaa tat gag	2949
Lys Leu Glu Met Ile Lys Pro Glu Glu Val Asn Leu Glu Glu Tyr Glu	
850 855 860 865	
gag tgg cat cag gat tat agg aaa ttc agg gaa aca act atg tat ctc	2997
Glu Trp His Gln Asp Tyr Arg Lys Phe Arg Glu Thr Thr Met Tyr Leu	
870 875 880	
ata att ggg cta gaa aat ttt caa aga gaa agt tat ata gat tcc ttg	3045
Ile Ile Gly Leu Glu Asn Phe Gln Arg Glu Ser Tyr Ile Asp Ser Leu	
885 890 895	
ctg ttc ctc atc tgt gct tat cag aat aac aaa gaa ctc ttg tct aaa	3093
Leu Phe Leu Ile Cys Ala Tyr Gln Asn Asn Lys Glu Leu Leu Ser Lys	
900 905 910	
ggc tta tac aga gga cat gat gaa gaa ttg ata tca cat tat aga aga	3141
Gly Leu Tyr Arg Gly His Asp Glu Glu Leu Ile Ser His Tyr Arg Arg	
915 920 925	
gaa tgt ttg cta atc ctt aat tta aaa agg aaa caa aaa cct att ctt	3189
Glu Cys Leu Leu Ile Leu Asn Leu Lys Arg Lys Gln Lys Pro Ile Leu	
930 935 940 945	
ttt ttt ttc ctg cat tgc att aag aaa tta aat gag caa gcc gca gaa	3237
Phe Phe Phe Leu His Cys Ile Lys Lys Leu Asn Glu Gln Ala Ala Glu	
950 955 960	
ctc ttc gaa tct gga gag gat cga gaa gta aac aat ggt ttg att atc	3285
Leu Phe Glu Ser Gly Glu Asp Arg Glu Val Asn Asn Gly Leu Ile Ile	
965 970 975	
atg aat gag ttt att gtc cca ttt ttg cca tta tta ctg gtg gat gaa	3333
Met Asn Glu Phe Ile Val Pro Phe Leu Pro Leu Leu Leu Val Asp Glu	
980 985 990	
atg gaa gaa aag gat ata cta gct gta gaa gat atg aga aat cga tgg	3381
Met Glu Glu Lys Asp Ile Leu Ala Val Glu Asp Met Arg Asn Arg Trp	
995 1000 1005	
tgt tcc tac ctt ggt caa gaa atg gaa cca cac ctc caa gaa aag	3426
Cys Ser Tyr Leu Gly Gln Glu Met Glu Pro His Leu Gln Glu Lys	
1010 1015 1020	
ctg aca gat ttt ttg cca aaa ctg ctt gat tgt tct atg gag att	3471
Leu Thr Asp Phe Leu Pro Lys Leu Leu Asp Cys Ser Met Glu Ile	
1025 1030 1035	
aaa agt ttc cat gag cca ccg aag tta cct tca tat tcc acg cat	3516
Lys Ser Phe His Glu Pro Pro Lys Leu Pro Ser Tyr Ser Thr His	



1040		1045		1050	
gaa ctc tgt gag cga ttt gcc cga atc atg ttg tcc ctc agt cga					3561
Glu Leu Cys Glu Arg Phe Ala Arg Ile Met Leu Ser Leu Ser Arg					
1055		1060		1065	
act cct gct gat gga aga taa actgcacact ttcctgaac aactgtata					3612
Thr Pro Ala Asp Gly Arg					
1070		1075			
aactcttttt agttcttaac ccttgccctc ctgtcacagg gtttgcttgt tgctgctata					3672
gtttttaact tttttttatt ttaataactg caaaagacaa aatgactata cagactttag					3732
tcagactgca gacaataaag ctgaaaatcg catggcgctc agacatttta accggaactg					3792
atgtataatc acaaatctaa ttgattttat tatggcaaaa ctatgctttt gccaccttcc					3852
tgttgcagta ttactttgct tttatctttt ctttctcaac agctttccat tcagtctgga					3912
tccttccatg actacagcca tttaagtgtt cagcactgtg tacgatacat aatatttgggt					3972
agcttgtaaa tgaaataaag aataaagttt tatttatggc tac					4015

Glu Glu Thr Thr Tyr Tyr Gln Thr Ala Leu Pro Gly Asn Asp Arg Tyr  
65 70 75 80

Ile Ser Val Gly Ser Gln Ala Asp Thr Asn Val Ile Asp Leu Thr Gly  
85 90 95

Asp Asp Lys Asp Asp Leu Gln Arg Thr Ile Ala Leu Ser Leu Ala Glu  
100 105 110

Ser Asn Arg Ala Phe Arg Glu Thr Gly Ile Thr Asp Glu Glu Gln Ala  
115 120 125

Ile Ser Arg Val Leu Glu Ala Ser Ile Ala Glu Asn Lys Ala Cys Leu  
130 135 140

Lys Arg Thr Pro Thr Glu Val Trp Arg Asp Ser Arg Asn Pro Tyr Asp  
145 150 155 160

Arg Lys Arg Gln Asp Lys Ala Pro Val Gly Leu Lys Asn Val Gly Asn  
165 170 175

Thr Cys Trp Phe Ser Ala Val Ile Gln Ser Leu Phe Asn Leu Leu Glu  
180 185 190

Phe Arg Arg Leu Val Leu Asn Tyr Lys Pro Pro Ser Asn Ala Gln Asp  
195 200 205

Leu Pro Arg Asn Gln Lys Glu His Arg Asn Leu Pro Phe Met Arg Glu  
210 215 220

Leu Arg Tyr Leu Phe Ala Leu Leu Val Gly Thr Lys Arg Lys Tyr Val  
225 230 235 240

Asp Pro Ser Arg Ala Val Glu Ile Leu Lys Asp Ala Phe Lys Ser Asn  
245 250 255

Asp Ser Gln Gln Gln Asp Val Ser Glu Phe Thr His Lys Leu Leu Asp  
260 265 270

Trp Leu Glu Asp Ala Phe Gln Met Lys Ala Glu Glu Glu Thr Asp Glu  
275 280 285

Glu Lys Pro Lys Asn Pro Met Val Glu Leu Phe Tyr Gly Arg Phe Leu  
 290 295 300

Ala Val Gly Val Leu Glu Gly Lys Lys Phe Glu Asn Thr Glu Met Phe  
 305 310 315 320

Gly Gln Tyr Pro Leu Gln Val Asn Gly Phe Lys Asp Leu His Glu Cys  
 325 330 335

Leu Glu Ala Ala Met Ile Glu Gly Glu Ile Glu Ser Leu His Ser Glu  
 340 345 350

Asn Ser Gly Lys Ser Gly Gln Glu His Trp Phe Thr Gly Leu Pro Pro  
 355 360 365

Val Leu Thr Phe Xaa Leu Ser Arg Phe Glu Phe Asn Gln Ala Leu Gly  
 370 375 380

Arg Pro Glu Lys Ile His Asn Lys Leu Glu Phe Pro Gln Val Leu Tyr  
 385 390 395 400

Leu Asp Arg Tyr Met His Arg Asn Arg Glu Ile Thr Arg Ile Lys Arg  
 405 410 415

Glu Glu Ile Lys Arg Leu Lys Asp Tyr Leu Thr Val Leu Gln Gln Arg  
 420 425 430

Leu Glu Arg Tyr Leu Ser Tyr Gly Ser Gly Pro Lys Arg Phe Pro Leu  
 435 440 445

Val Asp Val Leu Gln Tyr Ala Leu Glu Phe Ala Ser Ser Lys Pro Val  
 450 455 460

Cys Thr Ser Pro Val Asp Asp Ile Asp Ala Ser Ser Pro Pro Ser Gly  
 465 470 475 480

Ser Ile Pro Ser Gln Thr Leu Pro Ser Thr Thr Glu Gln Gln Gly Ala  
 485 490 495

Leu Ser Ser Glu Leu Pro Ser Thr Ser Pro Ser Ser Val Ala Ala Ile  
 500 505 510

Ser Ser Arg Ser Val Ile His Lys Pro Phe Thr Gln Ser Arg Ile Pro

515	520	525
Pro Asp Leu Pro Met His	Pro Ala Pro Arg His	Ile Thr Glu Glu Glu
530	535	540
Leu Ser Val Leu Glu Ser Cys	Leu His Arg Trp Arg Thr	Glu Ile Glu
545	550	555 560
Asn Asp Thr Arg Asp Leu Gln Glu Ser	Ile Ser Arg Ile His Arg Thr	
565	570	575
Ile Glu Leu Met Tyr Ser Asp Lys	Ser Met Ile Gln Val Pro Tyr Arg	
580	585	590
Leu His Ala Val Leu Val His Glu Gly Gln Ala	Asn Ala Gly His Tyr	
595	600	605
Trp Ala Tyr Ile Phe Asp His Arg Glu Ser Arg	Trp Met Lys Tyr Asn	
610	615	620
Asp Ile Ala Val Thr Lys Ser Ser Trp Glu Glu Leu Val Arg Asp Ser		
625	630	635 640
Phe Gly Gly Tyr Arg Asn Ala Ser Ala Tyr Cys Leu Met Tyr Ile Asn		
645	650	655
Asp Lys Ala Gln Phe Leu Ile Gln Glu Glu Phe Asn Lys Glu Thr Gly		
660	665	670
Gln Pro Leu Val Gly Ile Glu Thr Leu Pro Pro Asp Leu Arg Asp Phe		
675	680	685
Val Glu Glu Asp Asn Gln Arg Phe Glu Lys Glu Leu Glu Glu Trp Asp		
690	695	700
Ala Gln Leu Ala Gln Lys Ala Leu Gln Glu Lys Leu Leu Ala Ser Gln		
705	710	715 720
Lys Leu Arg Glu Ser Glu Thr Ser Val Thr Thr Ala Gln Ala Ala Gly		
725	730	735
Asp Pro Glu Tyr Leu Glu Gln Pro Ser Arg Ser Asp Phe Ser Lys His		
740	745	750

Leu Lys Glu Glu Thr Ile Gln Ile Ile Thr Lys Ala Ser His Glu His  
755 760 765

Glu Asp Lys Ser Pro Glu Thr Val Leu Gln Ser Ala Ile Lys Leu Glu  
770 775 780

Tyr Ala Arg Leu Val Lys Leu Ala Gln Glu Asp Thr Pro Pro Glu Thr  
785 790 795 800

Asp Tyr Arg Leu His His Val Val Val Tyr Phe Ile Gln Asn Gln Ala  
805 810 815

Pro Lys Lys Ile Ile Glu Lys Thr Leu Leu Glu Gln Phe Gly Asp Arg  
820 825 830

Asn Leu Ser Phe Asp Glu Arg Cys His Asn Ile Met Lys Val Ala Gln  
835 840 845

Ala Lys Leu Glu Met Ile Lys Pro Glu Glu Val Asn Leu Glu Glu Tyr  
850 855 860

Glu Glu Trp His Gln Asp Tyr Arg Lys Phe Arg Glu Thr Thr Met Tyr  
865 870 875 880

Leu Ile Ile Gly Leu Glu Asn Phe Gln Arg Glu Ser Tyr Ile Asp Ser  
885 890 895

Leu Leu Phe Leu Ile Cys Ala Tyr Gln Asn Asn Lys Glu Leu Leu Ser  
900 905 910

Lys Gly Leu Tyr Arg Gly His Asp Glu Glu Leu Ile Ser His Tyr Arg  
915 920 925

Arg Glu Cys Leu Leu Ile Leu Asn Leu Lys Arg Lys Gln Lys Pro Ile  
930 935 940

Leu Phe Phe Phe Leu His Cys Ile Lys Lys Leu Asn Glu Gln Ala Ala  
945 950 955 960

Glu Leu Phe Glu Ser Gly Glu Asp Arg Glu Val Asn Asn Gly Leu Ile  
965 970 975

Ile Met Asn Glu Phe Ile Val Pro Phe Leu Pro Leu Leu Leu Val Asp  
980 985 990

Glu Met Glu Glu Lys Asp Ile Leu Ala Val Glu Asp Met Arg Asn Arg  
995 1000 1005

Trp Cys Ser Tyr Leu Gly Gln Glu Met Glu Pro His Leu Gln Glu  
1010 1015 1020

Lys Leu Thr Asp Phe Leu Pro Lys Leu Leu Asp Cys Ser Met Glu  
1025 1030 1035

Ile Lys Ser Phe His Glu Pro Pro Lys Leu Pro Ser Tyr Ser Thr  
1040 1045 1050

His Glu Leu Cys Glu Arg Phe Ala Arg Ile Met Leu Ser Leu Ser  
1055 1060 1065

Arg Thr Pro Ala Asp Gly Arg  
1070 1075

<210> 5  
<211> 1075  
<212> PRT  
<213> Homo sapiens

<400> 5

Met Thr Val Glu Gln Asn Val Leu Gln Gln Ser Ala Ala Gln Lys His  
1 5 10 15

Gln Gln Thr Phe Leu Asn Gln Leu Arg Glu Ile Thr Gly Ile Asn Asp  
20 25 30

Thr Gln Ile Leu Gln Gln Ala Leu Lys Asp Ser Asn Gly Asn Leu Glu  
35 40 45

Leu Ala Val Ala Phe Leu Thr Ala Lys Asn Ala Lys Thr Pro Gln Gln  
50 55 60

Glu Glu Thr Thr Tyr Tyr Gln Thr Ala Leu Pro Gly Asn Asp Arg Tyr  
65 70 75 80

Ile Ser Val Gly Ser Gln Ala Asp Thr Asn Val Ile Asp Leu Thr Gly

85

90

95

Asp Asp Lys Asp Asp Leu Gln Arg Ala Ile Ala Leu Ser Leu Ala Glu  
 100 105 110

Ser Asn Arg Ala Phe Arg Glu Thr Gly Ile Thr Asp Glu Glu Gln Ala  
 115 120 125

Ile Ser Arg Val Leu Glu Ala Ser Ile Ala Glu Asn Lys Ala Cys Leu  
 130 135 140

Lys Arg Thr Pro Thr Glu Val Trp Arg Asp Ser Arg Asn Pro Tyr Asp  
 145 150 155 160

Arg Lys Arg Gln Asp Lys Ala Pro Val Gly Leu Lys Asn Val Gly Asn  
 165 170 175

Thr Cys Trp Phe Ser Ala Val Ile Gln Ser Leu Phe Asn Leu Leu Glu  
 180 185 190

Phe Arg Arg Leu Val Leu Asn Tyr Lys Pro Pro Ser Asn Ala Gln Asp  
 195 200 205

Leu Pro Arg Asn Gln Lys Glu His Arg Asn Leu Pro Phe Met Arg Glu  
 210 215 220

Leu Arg Tyr Leu Phe Ala Leu Leu Val Gly Thr Lys Arg Lys Tyr Val  
 225 230 235 240

Asp Pro Ser Arg Ala Val Glu Ile Leu Lys Asp Ala Phe Lys Ser Asn  
 245 250 255

Asp Ser Gln Gln Gln Asp Val Ser Glu Phe Thr His Lys Leu Leu Asp  
 260 265 270

Trp Leu Glu Asp Ala Phe Gln Met Lys Ala Glu Glu Glu Thr Asp Glu  
 275 280 285

Glu Lys Pro Lys Asn Pro Met Val Glu Leu Phe Tyr Gly Arg Phe Leu  
 290 295 300

Ala Val Gly Val Leu Glu Gly Lys Lys Phe Glu Asn Thr Glu Met Phe  
 305 310 315 320

Gly Gln Tyr Pro Leu Gln Val Asn Gly Phe Lys Asp Leu His Glu Cys  
 325 330 335

Leu Glu Ala Ala Met Ile Glu Gly Glu Ile Glu Ser Leu His Ser Glu  
 340 345 350

Asn Ser Gly Lys Ser Gly Gln Glu His Trp Phe Thr Glu Leu Pro Pro  
 355 360 365

Val Leu Thr Phe Glu Leu Ser Arg Phe Glu Phe Asn Gln Ala Leu Gly  
 370 375 380

Arg Pro Glu Lys Ile His Asn Lys Leu Glu Phe Pro Gln Val Leu Tyr  
 385 390 395 400

Leu Asp Arg Tyr Met His Arg Asn Arg Glu Ile Thr Arg Ile Lys Arg  
 405 410 415

Glu Glu Ile Lys Arg Leu Lys Asp Tyr Leu Thr Val Leu Gln Gln Arg  
 420 425 430

Leu Glu Arg Tyr Leu Ser Tyr Gly Ser Gly Pro Lys Arg Phe Pro Leu  
 435 440 445

Val Asp Val Leu Gln Tyr Ala Leu Glu Phe Ala Ser Ser Lys Pro Val  
 450 455 460

Cys Thr Ser Pro Val Asp Asp Ile Asp Ala Ser Ser Pro Pro Ser Gly  
 465 470 475 480

Ser Ile Pro Ser Gln Thr Leu Pro Ser Thr Thr Glu Gln Gln Gly Ala  
 485 490 495

Leu Ser Ser Glu Leu Pro Ser Thr Ser Pro Ser Ser Val Ala Ala Ile  
 500 505 510

Ser Ser Arg Ser Val Ile His Lys Pro Phe Thr Gln Ser Arg Ile Pro  
 515 520 525

Pro Asp Leu Pro Met His Pro Ala Pro Arg His Ile Thr Glu Glu Glu  
 530 535 540



Leu Ser Val Leu Glu Ser Cys Leu His Arg Trp Arg Thr Glu Ile Glu  
 545 550 555 560

Asn Asp Thr Arg Asp Leu Gln Glu Ser Ile Ser Arg Ile His Arg Thr  
 565 570 575

Ile Glu Leu Met Tyr Ser Asp Lys Ser Met Ile Gln Val Pro Tyr Arg  
 580 585 590

Leu His Ala Val Leu Val His Glu Gly Gln Ala Asn Ala Gly His Tyr  
 595 600 605

Trp Ala Tyr Ile Phe Asp His Arg Glu Ser Arg Trp Met Lys Tyr Asn  
 610 615 620

Asp Ile Ala Val Thr Lys Ser Ser Trp Glu Glu Leu Val Arg Asp Ser  
 625 630 635 640

Phe Gly Gly Tyr Arg Asn Ala Ser Ala Tyr Cys Leu Met Tyr Ile Asn  
 645 650 655

Asp Lys Ala Gln Phe Leu Ile Gln Glu Glu Phe Asn Lys Glu Thr Gly  
 660 665 670

Gln Pro Leu Val Gly Ile Glu Thr Leu Pro Pro Asp Leu Arg Asp Phe  
 675 680 685

Val Glu Glu Asp Asn Gln Arg Phe Glu Lys Glu Leu Glu Glu Trp Asp  
 690 695 700

Ala Gln Leu Ala Gln Lys Ala Leu Gln Glu Lys Leu Leu Ala Ser Gln  
 705 710 715 720

Lys Leu Arg Glu Ser Glu Thr Ser Val Thr Thr Ala Gln Ala Ala Gly  
 725 730 735

Asp Pro Glu Tyr Leu Glu Gln Pro Ser Arg Ser Asp Phe Ser Lys His  
 740 745 750

Leu Lys Glu Glu Thr Ile Gln Ile Ile Thr Lys Ala Ser His Glu His  
 755 760 765

Glu Asp Lys Ser Pro Glu Thr Val Leu Gln Ser Ala Ile Lys Leu Glu  
 770 775 780

Tyr Ala Arg Leu Val Lys Leu Ala Gln Glu Asp Thr Pro Pro Glu Thr  
 785 790 795 800

Asp Tyr Arg Leu His His Val Val Val Tyr Phe Ile Gln Asn Gln Ala  
 805 810 815

Pro Lys Lys Ile Ile Glu Lys Thr Leu Leu Glu Gln Phe Gly Asp Arg  
 820 825 830

Asn Leu Ser Phe Asp Glu Arg Cys His Asn Ile Met Lys Val Ala Gln  
 835 840 845

Ala Lys Leu Glu Met Ile Lys Pro Glu Glu Val Asn Leu Glu Glu Tyr  
 850 855 860

Glu Glu Trp His Gln Asp Tyr Arg Lys Phe Arg Glu Thr Thr Met Tyr  
 865 870 875 880

Leu Ile Ile Gly Leu Glu Asn Phe Gln Arg Glu Ser Tyr Ile Asp Ser  
 885 890 895

Leu Leu Phe Leu Ile Cys Ala Tyr Gln Asn Asn Lys Glu Leu Leu Ser  
 900 905 910

Lys Gly Leu Tyr Arg Gly His Asp Glu Glu Leu Ile Ser His Tyr Arg  
 915 920 925

Arg Glu Cys Leu Leu Ile Leu Asn Leu Lys Arg Lys Gln Lys Pro Ile  
 930 935 940

Leu Phe Phe Phe Leu His Cys Ile Lys Lys Leu Asn Glu Gln Ala Ala  
 945 950 955 960

Glu Leu Phe Glu Ser Gly Glu Asp Arg Glu Val Asn Asn Gly Leu Ile  
 965 970 975

Ile Met Asn Glu Phe Ile Val Pro Phe Leu Pro Leu Leu Leu Val Asp  
 980 985 990

Glu Met Glu Glu Lys Asp Ile Leu Ala Val Glu Asp Met Arg Asn Arg

995					1000					1005				
Trp	Cys	Ser	Tyr	Leu	Gly	Gln	Glu	Met	Glu	Pro	His	Leu	Gln	Glu
1010					1015					1020				
Lys	Leu	Thr	Asp	Phe	Leu	Pro	Lys	Leu	Leu	Asp	Cys	Ser	Met	Glu
1025					1030					1035				
Ile	Lys	Ser	Phe	His	Glu	Pro	Pro	Lys	Leu	Pro	Ser	Tyr	Ser	Thr
1040					1045					1050				
His	Glu	Leu	Cys	Glu	Arg	Phe	Ala	Arg	Ile	Met	Leu	Ser	Leu	Ser
1055					1060					1065				
Arg	Thr	Pro	Ala	Asp	Gly	Arg								
1070					1075									